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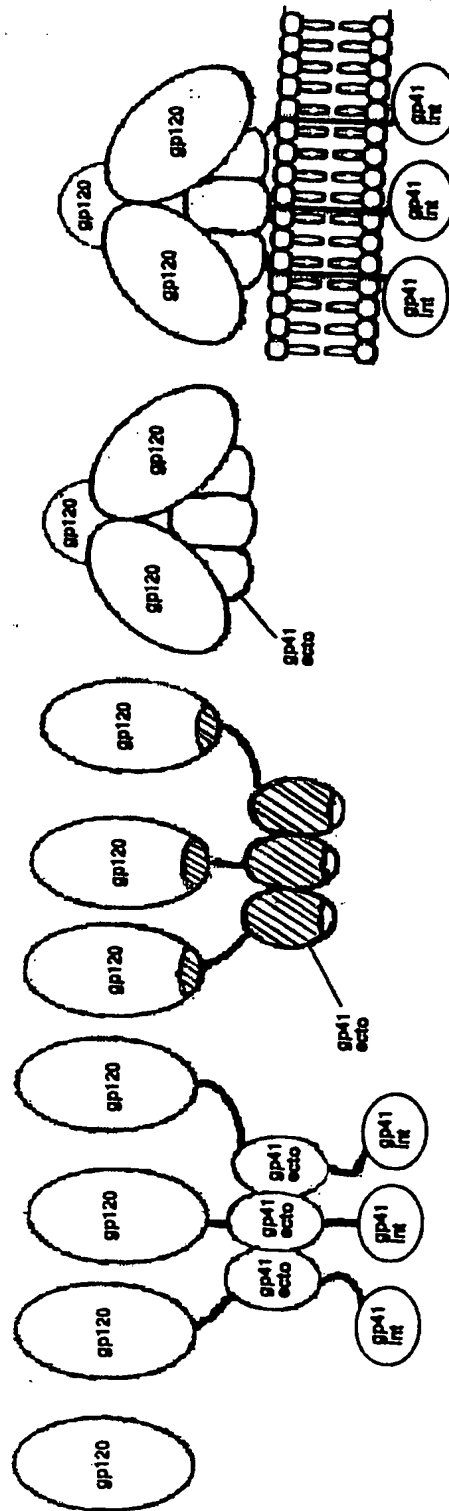
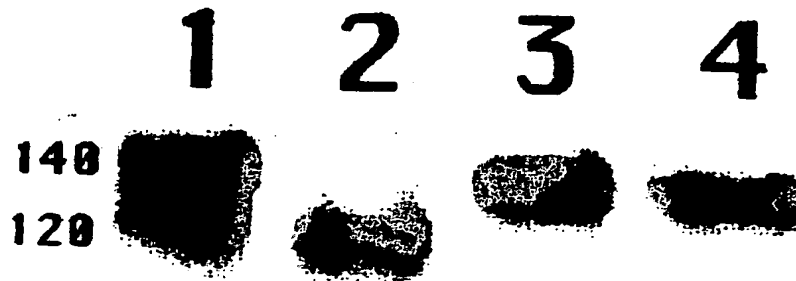


FIGURE 1

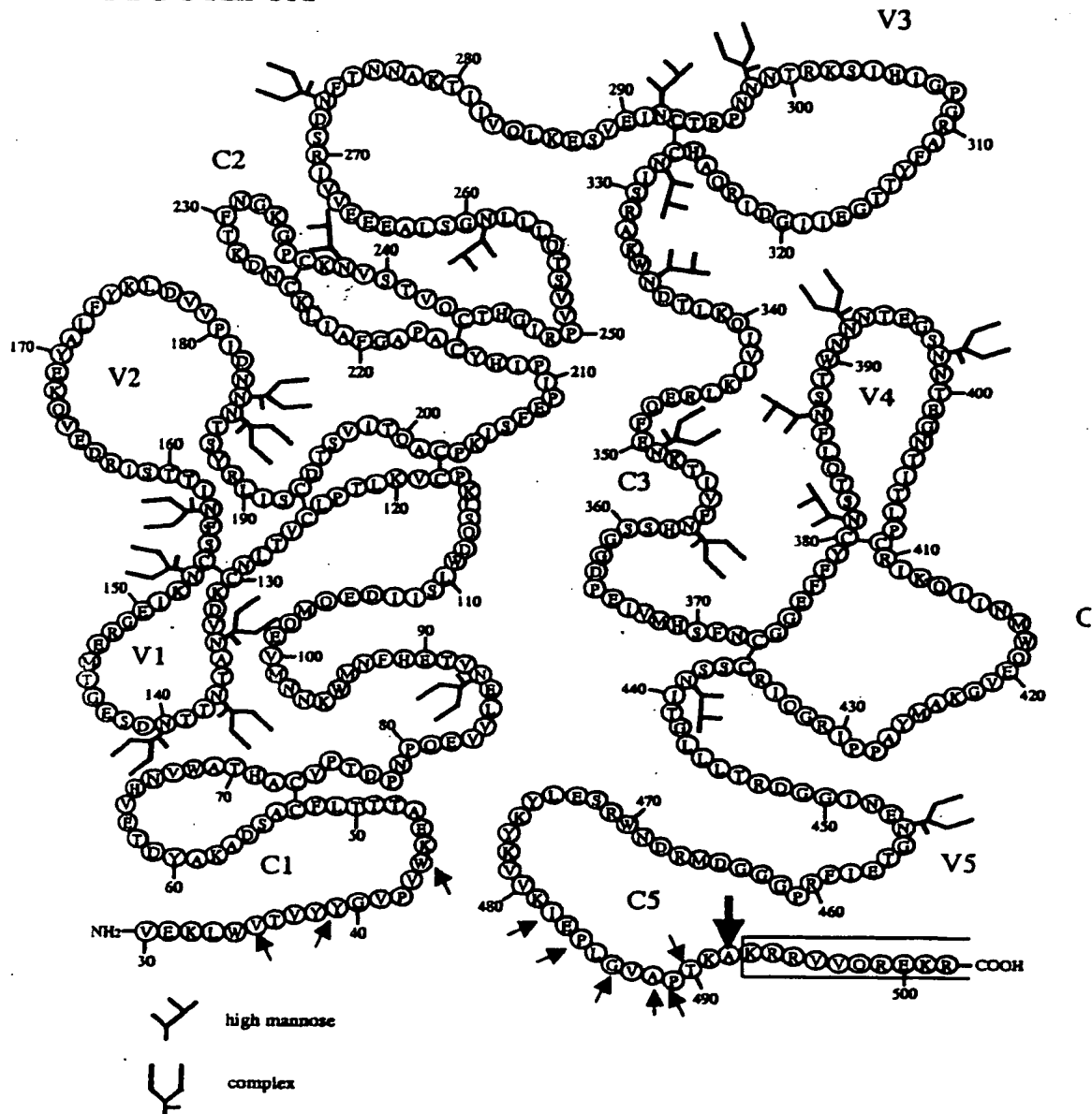
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FIGURE 2



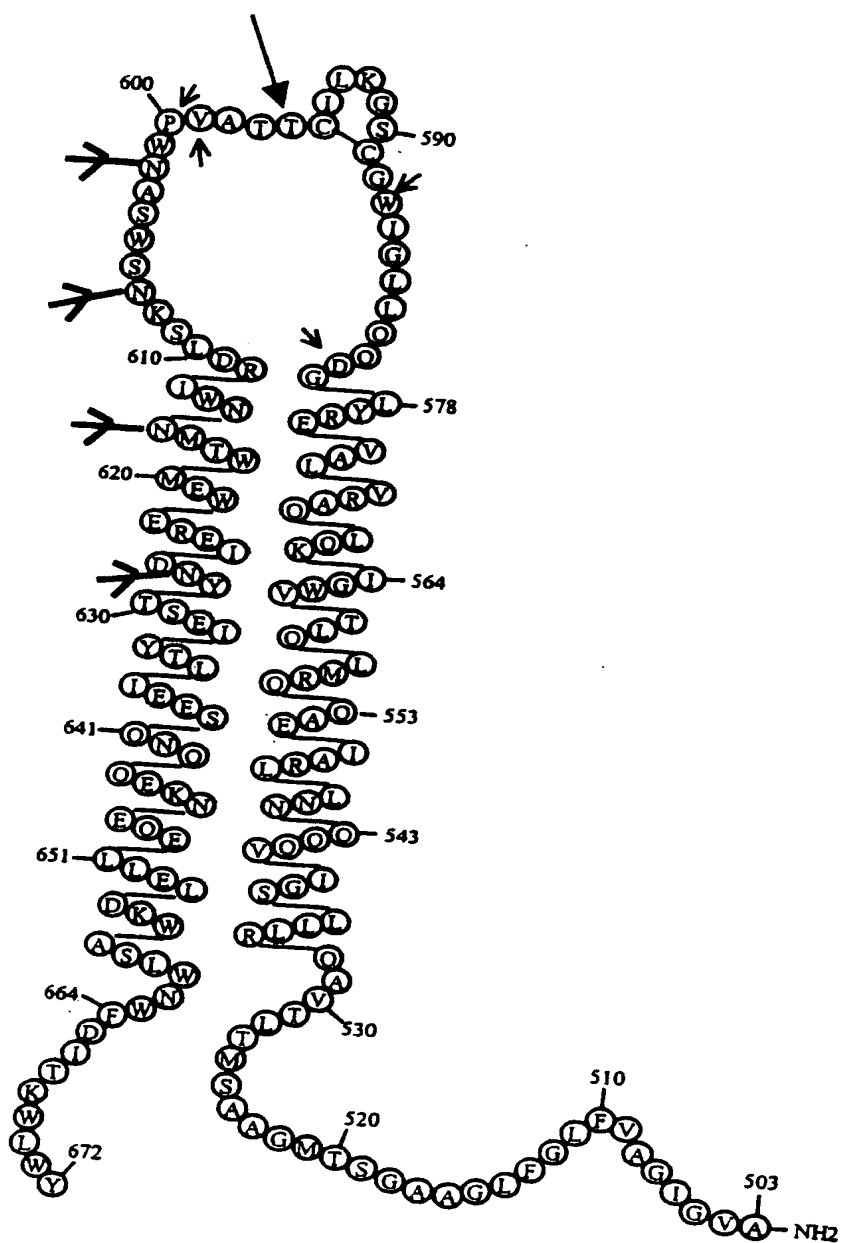
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FIGURE 3A



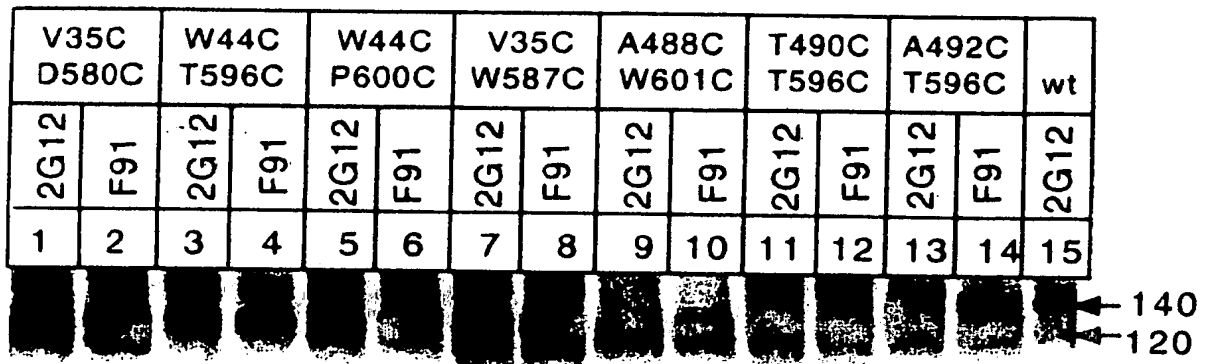
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FIGURE 3B



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FIGURE 4



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FIGURE 5

gp41							gp120		C1	
	D580C	W587C	T596C	V599C	P600C	W601C				
V35C	0.45	0.40	0.35	0.30	0.40	0.30				
Y39C	0.35	0.30	0.60	0.45	0.45	N.D.				
W44C	0.45	0.45	0.65	0.50	0.65	0.45				

gp120							C5	
	D580C	W587C	T596C	V599C	P600C	W601C		
P484C	0.35	0.30	0.45	0	0	0		
G486C	0	0	0.25	0.20	0.30	0		
A488C	0	0	0.05	0	0	0		
P489C	0	0.10	0.30	0.15	0.05	0		
T490C	0	0.15	0.55	0.25	0.25	0.10		
A492C	0.05	0	0.75	0.50	0.10	0.25		

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FIGURE 6A

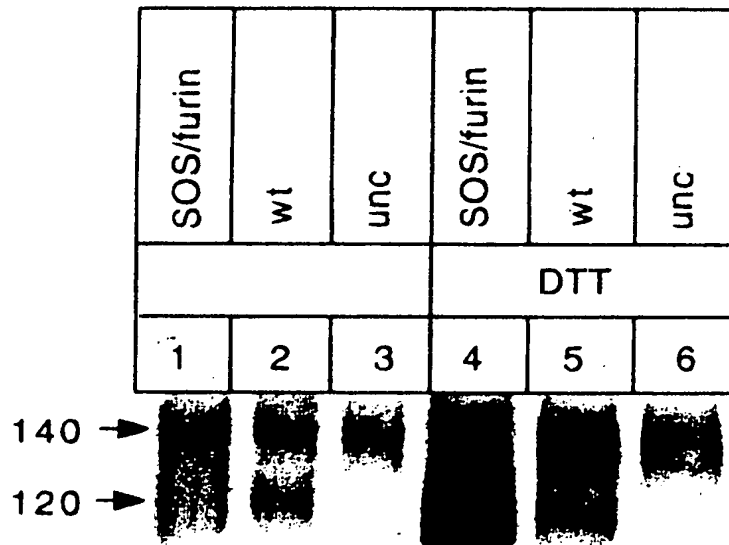


FIGURE 6B

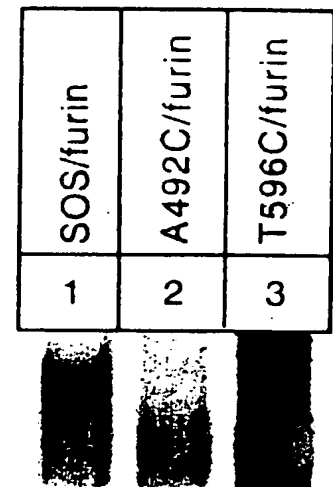
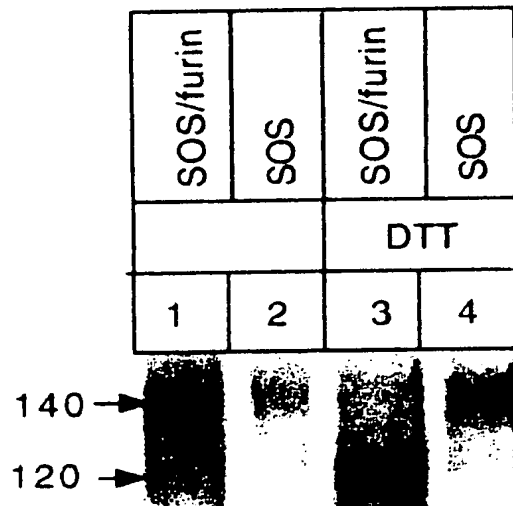


FIGURE 6C



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FIGURE 7

								K491A	K493A	K491A, K493A			
490, 596	491, 596	492, 596 (SOS)	493, 596	494, 596	495, 596	496, 596	498, 596	492, 596 (SOS)	492, 596 (SOS)	492, 596 (SOS)	44, 600; 491, 596	44, 600; 492, 596	44, 600; 493, 596
1	2	3	4	5	6	7	8	9	10	11	12	13	14

140 →

120 →

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FIGURE 8A

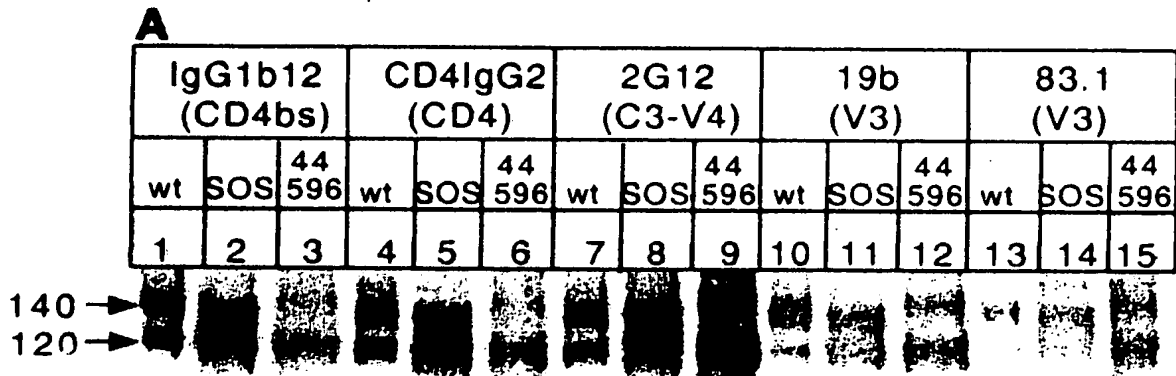


FIGURE 8B

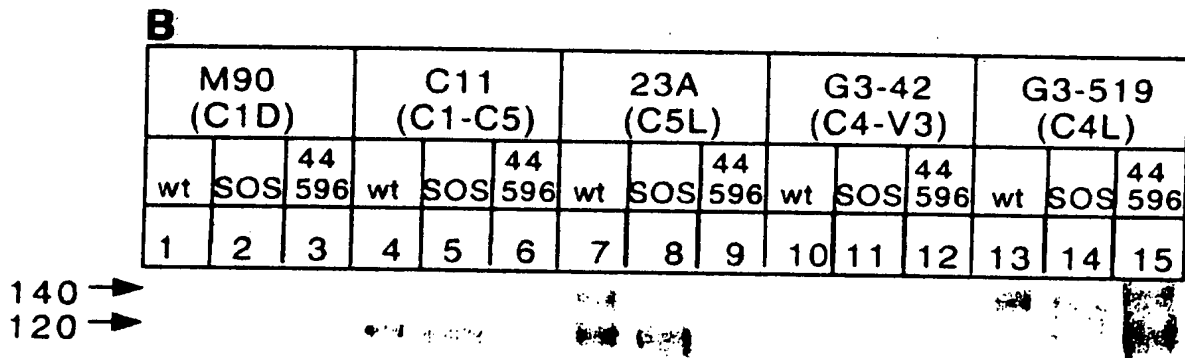
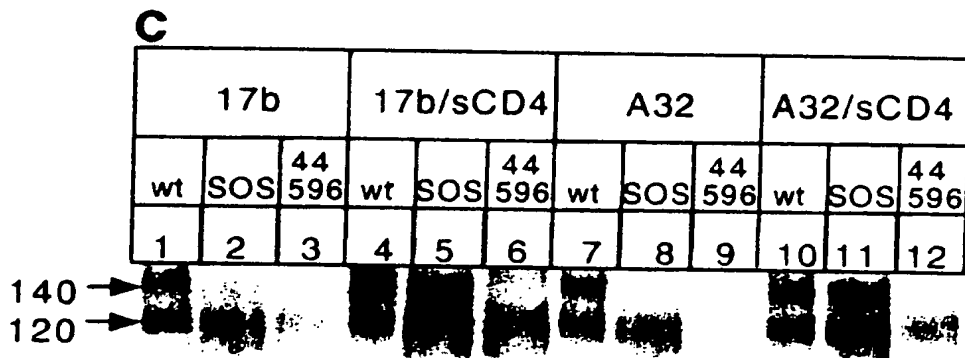


FIGURE 8C



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FIGURE 8D

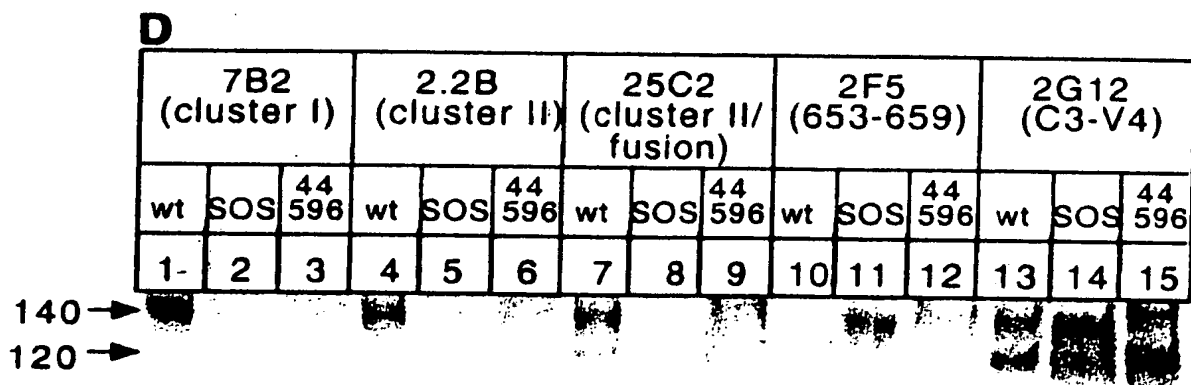
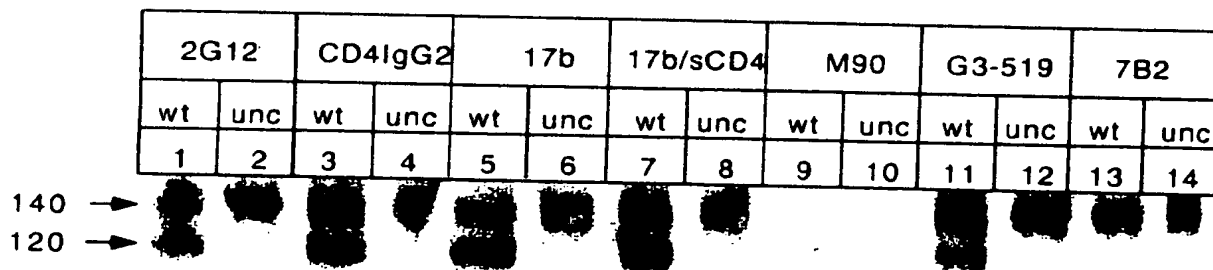


FIGURE 8E



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FIGURE 9A

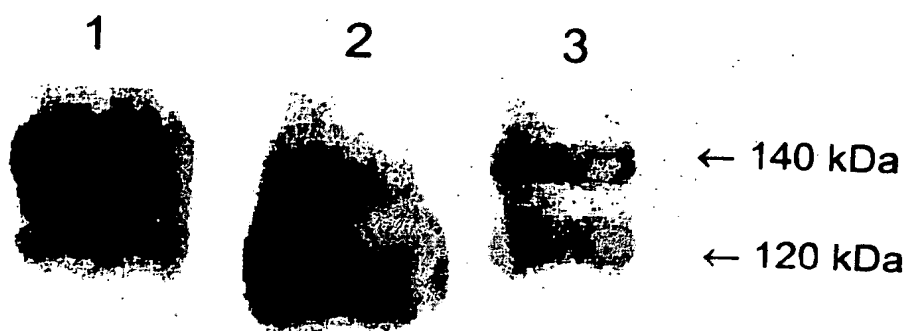


FIGURE 9B

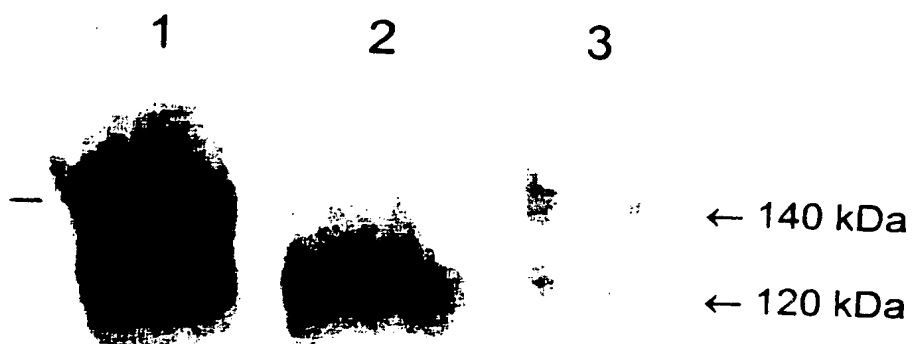
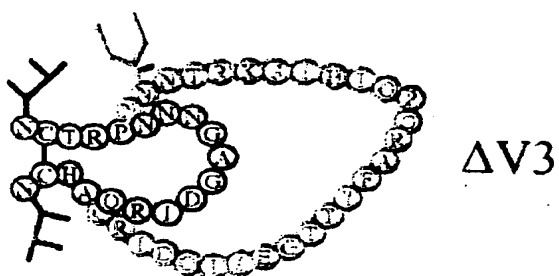
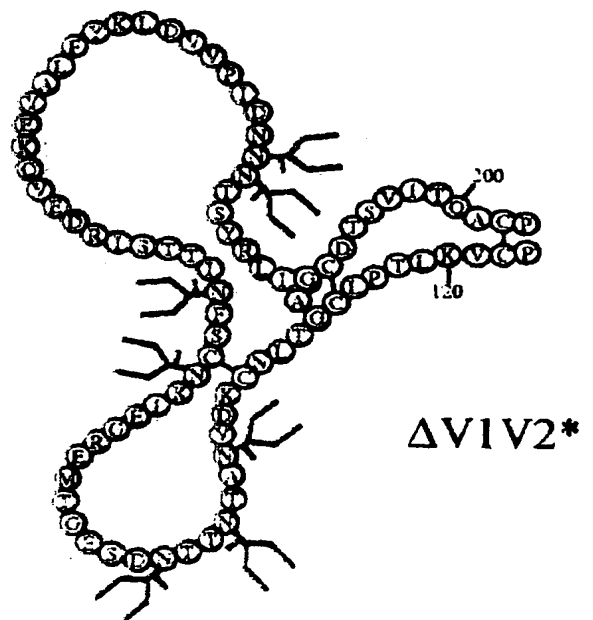
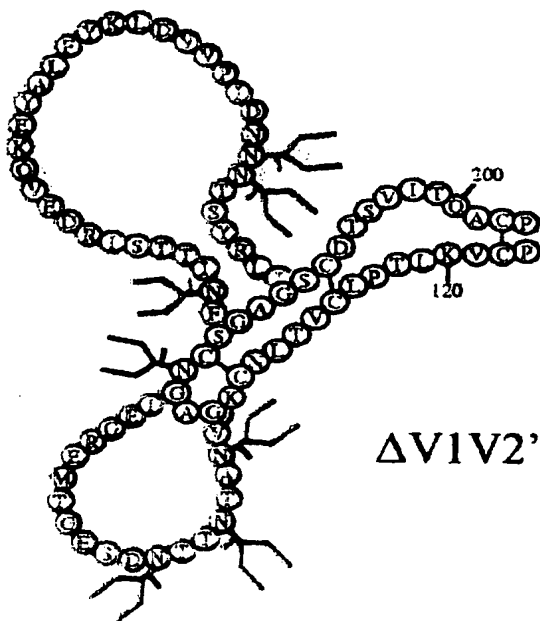
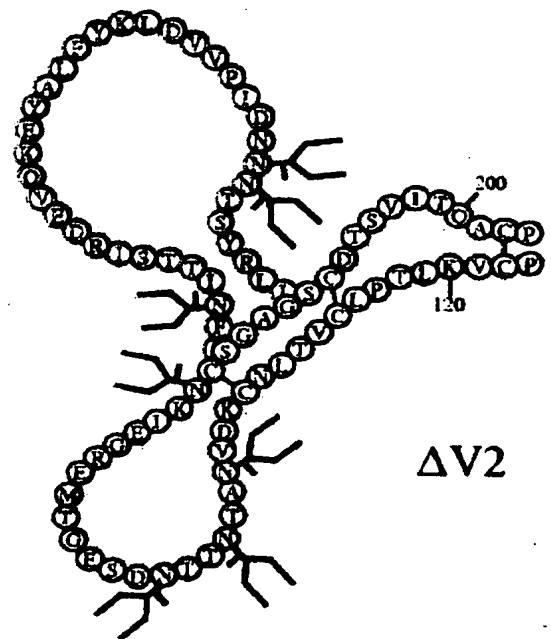
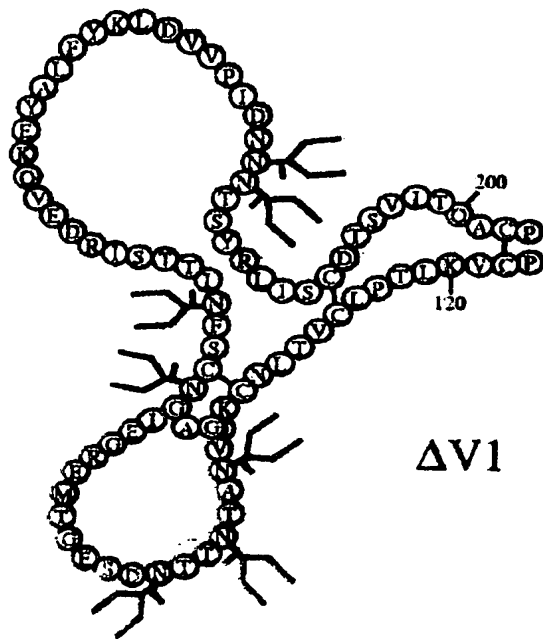


FIGURE 10

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FIGURE 11A

A

wt $\Delta VIV2^*V3$		CC $\Delta VIV2^*V3$		wt $\Delta VIV2^*V3$ N357Q N398Q		CC $\Delta VIV2^*V3$ N357Q N398Q		wt		envelope protein
2G12	F91	2G12	F91	2G12	F91	2G12	F91	F91	F91	antibody
1	2	3	4	5	6	7	8	9	10	lane

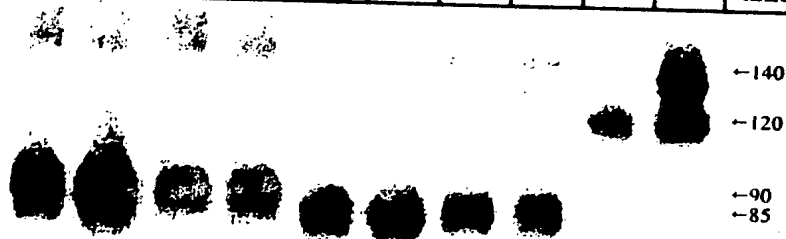
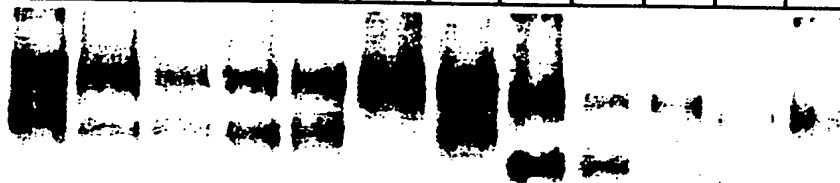


FIGURE 11B

B

wt	$\Delta V1$		$\Delta V2$		$\Delta V3$		$\Delta VIV2^*$		$\Delta VIV2^*$		$\Delta VIV2^*V3$		protein
CC		CC		CC		CC		CC		CC		CC	cysteines
1	2	3	4	5	6	7	8	9	10	11	12	13	lane



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FIGURE 12A

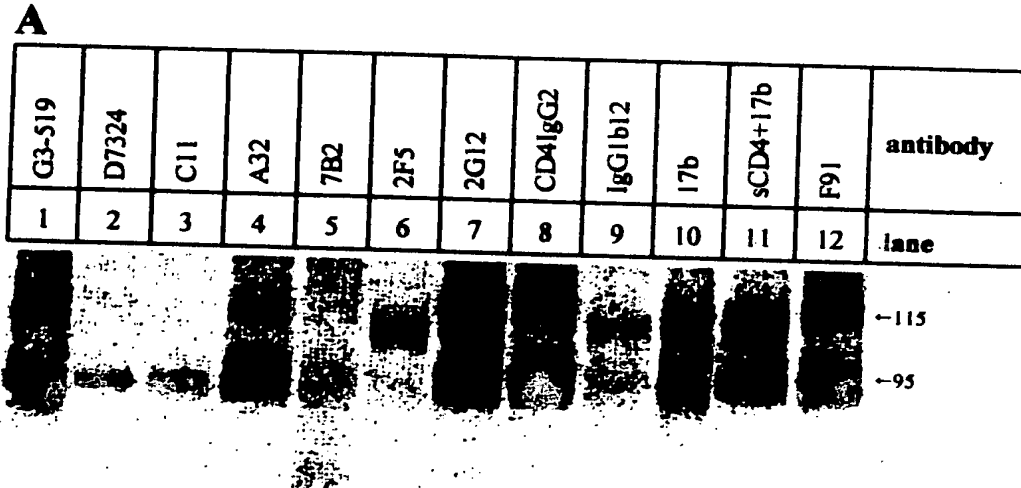
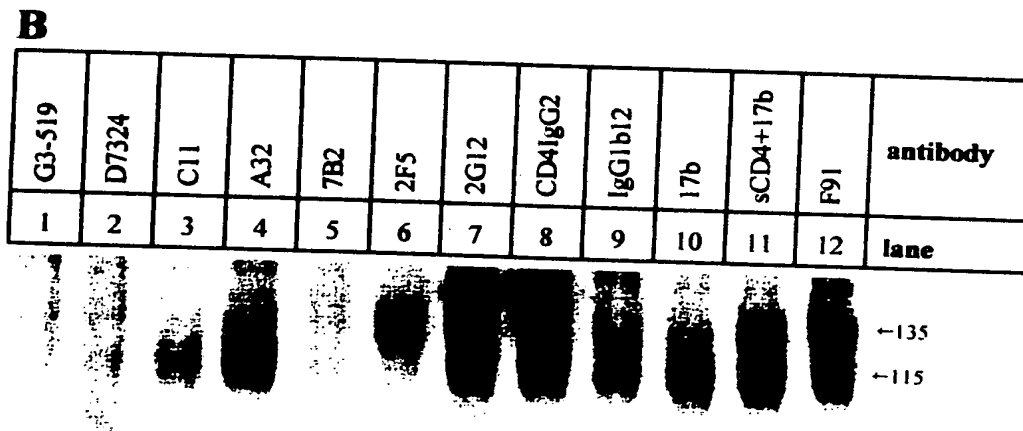


FIGURE 12B



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FIGURE 13A

HIV-1_{JR-FL} SOS gp140 (SEQ ID NO:12)

(a)

```
1   GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51  AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAATGTAACAGAACATTTTAAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAAT
301 TGCAAGGATGTGAATGCTACTAATACCACTAATGATAGCGAGGGAACGAT
351 GGAGAGAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAGCATAA
401 GAGATGAGGTGCAGAAAGAATATGCTCTTTTTTATAAACTTGATGTAGTA
451 CCAATAGATAATAATAATACCAGCTATAGGTTGATAAGTTGTGACACCTC
501 AGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAATTCCCATAC
551 ATTATTGTGCCCCGGCTGGTTTTGCGATTCTAAAGTGTAATGATAAGACG
601 TTCAATGGAAAAGGACCATGTAAATGTGAGCAGTACAATGTACACA
651 TGGAAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGGCAGTCTAG
701 CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACAATGCTAAA
751 ACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTACAAGACC
801 CAACAACAATACAAGAAAAAGTATACATATAGGACCAGGGAGAGCATTTT
851 ATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAAACAT
901 AGTAGAGCAAAATGGAATGACACTTTAAACAGATAGTTATAAAATTAAG
951 AGAACAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGG
1001 ACCCAGAAATTGTAATGCACAGTTTTTAATTGTGAAGGAGAATTTTTCTAC
1051 TGTAATTCAACACAACCTGTTTAATAGTACTTGAATAATAATACTGAAGG
1101 GTCAAATAACACTGAAGGAAATACTATCACACTCCCATGCAGAATAAAAC
1151 AAATTATAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCCTCCC
1201 ATCAGAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTATTAAC
1251 AAGAGATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAGACCTGGAG
1301 GAGGAGATATGAGGGACAATTGGAGAAGTGAATTCTATAAATATAAAGTA
1351 GTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGT
1401 GGTGCAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCTTGGGT
1451 TCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACG
1501 GTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGAACAAATTT
1551 GCTGAGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCACAGTCTGGG
1601 GCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGATACCTAGGG
1651 GATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACCTATTTGCTG
1701 CACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCTAGATAGGA
1751 TTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTAC
1801 ACAAGCGAAATATACACACTAATTGAAGAATCGCAGAACCAACAAGAAAA
1851 GAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATT
1901 GGTGTGACATAACAACTGGCTGTGGTAT
```

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FIGURE 13B

(SEQ ID NO:13)

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCVTLN
130	CKDVNATNTT	NDSEGTMERG	EIKNCSFNIT	TSIRDEVQKE	YALFYKLDVV
180	PIDNNNTSYR	LISCDTSVIT	QACPKISFEP	IPIHYCAPAG	FAILKCNDKT
230	FNGKGPCKNV	STVQCTHGIR	PVVSTQLLLN	GSLAEDEVVI	RSDNETNNAK
280	TIIVQLKESV	EINCTRPNNN	TRKSIHIGPG	RAFYTTEGII	GDIRQAHCNI
330	SRAKWNDTLK	QIVIKLREQF	ENKTIVFNHS	SGGDPEIVMH	SFNCEGEFFY
380	CNSTQLFNST	WNNNTEGSNN	TEGNTITLPC	RIKQIINMWQ	EVGKAMYAPP
430	IRGQIRCSSN	ITGLLLTRDG	GINENGTEIF	RPGGGDMRDN	WRSEFYKYKV
480	VKIEPLGVAP	TKCKRRVVQR	EKRAVGIGAV	FLGFLGAAGS	TMGAASMTLT
530	VQARLLLSGI	VQQQNNLLRA	IEAQQRMLQL	TVWGIKQLQA	RVLAVERYLG
580	DQQLLGIWGC	SGKLICTAV	PWNASWSNKS	LDRIWNNMTW	MEWEREIDNY
630	TSEIYTLIEE	SONQOEKNEQ	ELLELDKWAS	LWNWFDITNW	LWY

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FIGURE 14A

HIV-1_{JR-FL} ΔV1V2* SOS gp140 (SEQ ID NO:14)

(a)

```
1   GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51  AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAAAATGTAACAGAACATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGGTGCAGGATGT
301 GACACCTCAGTCATTACACAGGCCCTGTCCAAAGATATCCTTTGAGCCAAAT
351 TCCCATACATTATTGTGCCCGGCTGGTTTTGCGATTCTAAAGTGTAATG
401 ATAAGACGTTCAATGGAAAAGGACCATGTAAAAATGTCAGCACAGTACAA
451 TGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGG
501 CAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACA
551 ATGCTAAAACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGT
601 ACAAGACCCAACAACAATACAAGAAAAGTATACATATAGGACCAGGGAG
651 AGCATTTTATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATT
701 GTAACATTAGTAGAGCAAAATGGAATGACACTTTAAAACAGATAGTTATA
751 AAATTAAGAGAACAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTC
801 AGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTGTGGAGGAGAAT
851 TTTTCTACTGTAATTCAACACAACAGTGTTAATAGTACTTGGAATAATAAT
901 ACTGAAGGGTCAAATAACACTGAAGGAAATACTATCACACTCCCATGCAG
951 AATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATG
1001 CCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTG
1051 CTATTAACAAGAGATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAG
1101 ACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAAT
1151 ATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAG
1201 AGAAGAGTGGTGCAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTT
1251 CCTTGGGTTCCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGA
1301 CACTGACGGTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAG
1351 AACAATTTGCTGAGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCAC
1401 AGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGAT
1451 ACCTAGGGGATCAACAGCTCCTGGGGATTGTTGGGTTGCTCTGGAAAACCTC
1501 ATTTGCTGCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCT
1551 GGATAGGATTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTG
1601 ACAATTACACAAGCGAAATATACACCCTAATTGAAGAATCGCAGAACCAA
1651 CAAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTT
1701 GTGGAATTGGTTTGACATAACAACTGGCTGTGGTAT
```

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FIGURE 14B

(SEQ ID NO:15)

(b)
30 VEKLWVTVYY GVPVWKEATT TLFCASDAKA YDTEVHNVWA THACVPTDPN
80 PQEVVLENTV EHFNMWKNNM VEQMQEDIIS LWDQSLKPCV KLTPLCGAGC
130 DTSVITQACP KISFEPIPIH YCAPAGFAIL KCNDKTFNGK GPCKNVSTVQ
180 CTHGIRPVVS TQLLLNGSLA EEEVVIRSDN FTNNAKTIIV QLKESVEINC
230 TRPNNNTRKS IHIGPGRAFY TTGEIIGDIR QAHCNISRAK WNDTLKQIVI
280 KLREQFENKT IVFNHSSGGD PEIVMHSFNC GGEFFYCNST QLFNSTWNNN
330 TEGSNNTTEGN TITLPCRIKQ IINMWQEVGK AMYAPPIRGQ IRCSSNITGL
380 LLTRDGGINE NGTEIFRPGG GDMRDNRWSE LYKYKVVKIE PLGVAPTKCK
430 RRVVQREKRA VGIGAVFLGF LGAAGSTMGA ASMTLTVQAR LLLSGIVQQQ
480 NNLLRAIEAQ QRMLQLTVWG IKQLQARVLA VERYLGDOQL LGIWGCSGKL
530 ICCTAVPWNA SWSNKSLDRI WNNMTWMEWE REIDNYTSEI YTLIEESQNO
580 QEKNEQELLE LDKWASLWNW FDITNWLWY

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FIGURE 15A

HIV-1_{JR-FL} ΔV3 SOS gp140 (SEQ ID NO:16)

(a)

```
1   GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51  AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAAAATGTAACAGAACATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAAT
301 TGCAAGGATGTGAATGCTACTAATACCACTAATGATAGCGAGGGAACGAT
351 GGAGAGAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAGCATAA
401 GAGATGAGGTGCAGAAAGAATATGCTCTTTTTTATAAACTTGATGTAGTA
451 CCNATAGATAATAATAATACCAGCTATAGGTTGATAAGTTGTGACACCTC
501 AGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAATTCCCATAC
551 ATTATTGTGCCCCGGCTGGTTTTTGCATTCTAAAGTGTAATGATAAGACG
601 TTCAATGGAAAAGGNCCATGTAAAAATGTCAGCACAGTNCAATGTACACA
651 TGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGGCAGTCTAG
701 CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACAATGCTAAA
751 ACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTACAAGACC
801 CAACAACAATGGAGCCGGCGATATAAGACAAGCACATTGTAACATTAGTA
851 GAGCAAAATGGAATGACACTTTAAAACAGATAGTTATAAAATTAAGAGAA
901 CAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGACCC
951 AGAAATTGTAATGCACAGTTTTTAATTGTGGAGGAGAATTTTTCTACTGTA
1001 ATTCAACACAACCTGTTTAATAGTACTTGGAATAATAATACTGAAGGGTCA
1051 AATAACACTGAAGGAAATACTATCACACTCCCATGCAGAATAAAACAAAT
1101 TATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCCTCCCATCA
1151 GAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTATTAACAAGA
1201 GATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAGACCTGGAGGAGG
1251 AGATATGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAA
1301 AAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGTGGTG
1351 CAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCCCTGGGTTCTT
1401 GGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACGGTAC
1451 AGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGAACAATTTGCTG
1501 AGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCACAGTCTGGGGCAT
1551 CAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGATACCTAGGGGATC
1601 AACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACCTATTTGCTGCACT
1651 GCTGTGCCTTGAATGCTAGTTGGAGTAATAAATCTCTGGATAGGATTTG
1701 GAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTACACAA
1751 GCGAAATATACACCCTAATTGAAGAATCGCAGAACCAACAAGAAAAGAAT
1801 GAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTT
1851 TGACATAACAAAATGGCTGTGGTAT
```

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FIGURE 15B

(SEQ ID NO:17)

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCVTLN
130	CKDVNATNTT	NDSEGTMERG	EIKNCSFNIT	TSIRDEVQKE	YALFYKLDVV
180	XIDNNNTSYR	LISCDTSVIT	QACPKISFEP	IPIHYCAPAG	FAILKCNDKT
230	FNGKXPCKNV	STXQCTHGIR	PVVSTQLLLN	GSLAEEEVVI	RSDNFTNNAK
280	TIIVQLKESV	EINCTRPNNN	GAGDIRQAHC	NISRAKWNDT	LKQIVIKLRE
330	QFENKTIVFN	HSSGGDPEIV	MHSFNCGGEF	FYCNSTQLFN	STWNNNTEGS
380	NNTEGNTITL	PCRIKQIINM	WQEVGKAMYA	PPIRGQIRCS	SNITGLLLTR
430	DGGINENGTE	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKCKRRVV
480	QREKRAVGIG	AVFLGFLGAA	GSTMGAASMT	LTVQARLLLS	GIVQQQNNLL
530	RAIEAQQRML	QLTVWGIKQL	QARVLAVERY	LGDOQLLGIW	GCSGKLICCT
580	AVPWNASWSN	KSLDRIWNNM	TWMEWEREID	NYTSEIYTTLI	EESQNQQEKN
630	EQELLELDKW	ASLWNWFDIT	KWLWY		